

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bartley, Timothy D.  
Bogenberger, Jakob M.  
Rosselman, Robert A.  
Hunt, Pamela  
Kinstler, Olaf B.  
Samal, Babru B.

(ii) TITLE OF INVENTION: Compositions and Methods for Stimulating  
Megakaryocyte Growth and Differentiation

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.  
(B) STREET: 1840 Dehavilland Drive  
(C) CITY: Thousand Oaks  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cook, Robert R.  
(C) REFERENCE/DOCKET NUMBER: A-290-C

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp  
1 5 10 15

Ser His Val Leu His Xaa Arg Leu Xaa Gln Xaa Pro Asp Ile Tyr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp  
1 5 10 15

Ser His Val Leu His  
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Gln Lys Glu Gln Thr Lys Ala Gln Asp Val Leu Gly Ala Val Ala  
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCNCCNCCNG CNTGYGA

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCARTGYAAC ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp  
1 5 10 15  
Ser His Val Leu His  
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTACGCGTTC TAGANNNNNN T

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTTTACTGA GGACTCGGAG G

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

29

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGACCTCC GAGTCCTCAG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTCCTCAG TAAACTGCTT CGT

23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGTCACGA AGCAGTTTAC

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTTTACTTC TAGGCCTG

18

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGTCACAA GCAGGAGGA

19

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCATAGTCC GGGACGTCG

19

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCCTCCTGCT TGTGACCTC

19

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGGAAGGA TTCAGGGGA

19

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAACAAGTCG ACCGCCAGCC AGACACCCCG

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGGATAG GCCACTCNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCARTGYAAN ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGGTGTGCA CTTGTG

16

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACAAGTGCA CACCAACCCC

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1342 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 99..1094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGAGCCA CGCCAGCCAA GACACCCCGG CCAGATGGA GCTGACTGAA TTGCTCCTCG

60

TGGTCATGCT TCTCCTAACT GCAAGGCTAA CGCTGTCC AGC CCG GCT CCT CCT  
Ser Pro Ala Pro Pro  
1 5

113



GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC 161  
 Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val  
 10 15 20  
 CTT CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA 209  
 Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr  
 25 30 35  
 CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC 257  
 Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr  
 40 45 50  
 CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT 305  
 Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu  
 55 60 65  
 CTG CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC 353  
 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys  
 70 75 80 85  
 CTC TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT 401  
 Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu  
 90 95 100  
 GGG GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 449  
 Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg  
 105 110 115  
 ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC 497  
 Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His  
 120 125 130  
 CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC 545  
 Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr  
 135 140 145  
 CTC TGC GTC AGG CGG GCC CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC 593  
 Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr  
 150 155 160 165  
 TCT CTA GTC CTC ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG 641  
 Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu  
 170 175 180  
 TTG GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT GGG CTT 689  
 Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu  
 185 190 195  
 CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT CCT GGT CTG CTG AAC 737  
 Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn  
 200 205 210  
 CAA ACC TCC AGG TCC CTG GAC CAA ATC CCC GGA TAC CTG AAC AGG ATA 785  
 Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile  
 215 220 225

CAC GAA CTC TTG AAT GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC 833  
 His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg  
 230 235 240 245  
 AGG ACC CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA GGC 881  
 Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly  
 250 255 260  
 TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT TCC CCA ACC CAT 929  
 Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His  
 265 270 275  
 CCT CCT ACT GGA CAG TAT ACG CTC TTC CCT CTT CCA CCC ACC TTG CCC 977  
 Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro  
 280 285 290  
 ACC CCT GTG GTC CAG CTC CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA 1025  
 Thr Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro  
 295 300 305  
 ACG CCC ACC CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1073  
 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser  
 310 315 320 325  
 CAG AAT CTG TCT CAG GAA GGG TAAGCTTCTC AGACACTGCC GACATCAGCA 1124  
 Gln Asn Leu Ser Gln Glu Gly 330  
 TTGTCTCGTG TACAGCTCCC TTCCCTGCAG GGCGCCCTG GGAGACAACT GGACAAGATT 1184  
 TCCTACTTTC TCCTGAAACC CAAAGCCCTG GTAAAAGGGA TACACAGGAC TGAAAAGGGA 1244  
 ATCATTTTTC ACTGTACATT ATAAACCTTC AGAAGCTATT TTTTAAAGCT ATCAGCAATA 1304  
 CTCATCAGAG CAGCTAGCTC TTTGGTCTAT TTTCTGCA 1342

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
 1 5 10 15  
 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
 20 25 30  
 His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
 35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
 50 55 60  
 Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
 65 70 75 80  
 Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln  
 85 90 95  
 Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu  
 100 105 110  
 Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe  
 115 120 125  
 Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
 130 135 140  
 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala  
 145 150 155 160  
 Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn  
 165 170 175  
 Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr  
 180 185 190  
 Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile  
 195 200 205  
 Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly  
 210 215 220  
 Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe  
 225 230 235 240  
 Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly  
 245 250 255  
 Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser  
 260 265 270  
 Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu  
 275 280 285  
 Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His Pro Leu Leu Pro  
 290 295 300  
 Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr  
 305 310 315 320  
 Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly  
 325 330

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1342 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 99..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGGGAGCCA	CGCCAGCCAA	GACACCCGG	CCAGAATGGA	GCTGACTGAA	TTGCTCCTCG		60									
TGGTCATGCT	TCTCCTAACT	GCAAGGCTAA	CGCTGTCC	AGC	CCG	GCT	CCT	CCT								113
										Ser	Pro	Ala	Pro	Pro		5
										1						
GCT	TGT	GAC	CTC	CGA	GTC	CTC	AGT	AAA	CTG	CTT	CGT	GAC	TCC	CAT	GTC	161
Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	
				10					15					20		
CTT	CAC	AGC	AGA	CTG	AGC	CAG	TGC	CCA	GAG	GTT	CAC	CCT	TTG	CCT	ACA	209
Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	
			25					30					35			
CCT	GTC	CTG	CTG	CCT	GCT	GTG	GAC	TTT	AGC	TTG	GGA	GAA	TGG	AAA	ACC	257
Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	
		40					45					50				
CAG	ATG	GAG	GAG	ACC	AAG	GCA	CAG	GAC	ATT	CTG	GGA	GCA	GTG	ACC	CTT	305
Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	
	55					60					65					
CTG	CTG	GAG	GGA	GTG	ATG	GCA	GCA	CGG	GGA	CAA	CTG	GGA	CCC	ACT	TGC	353
Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	
	70				75				80						85	
CTC	TCA	TCC	CTC	CTG	GGG	CAG	CTT	TCT	GGA	CAG	GTC	CGT	CTC	CTC	CTT	401
Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	
				90					95					100		
GGG	GCC	CTG	CAG	AGC	CTC	CTT	GGA	ACC	CAG	CTT	CCT	CCA	CAG	GGC	AGG	449
Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	
			105					110					115			
ACC	ACA	GCT	CAC	AAG	GAT	CCC	AAT	GCC	ATC	TTC	CTG	AGC	TTC	CAA	CAC	497
Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	
		120					125					130				

TG CTC CGA GGA AAG GTG CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC 545  
 Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr  
 135 140 145  
 CTC TGC GTC AGG CGG GCC CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC 593  
 Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr  
 150 155 160 165  
 TCT CTA GTC CTC ACA CTG AAC GAG CTC C CAAACAGGAC TTCTGGATTG 641  
 Ser Leu Val Leu Thr Leu Asn Glu Leu  
 170  
 TTGGAGACAA ACTTCACTGC CTCAGCCAGA ACTACTGGCT CTGGGCTTCT GAAGTGGCAG 701  
 CAGGGATTCA GAGCCAAGAT TCCTGGTCTG CTGAACCAAA CCTCCAGGTC CCTGGACCAA 761  
 ATCCCCGGAT ACCTGAACAG GATACACGAA CTCTTGAATG GAACTCGTGG ACTCTTTTCT 821  
 GGACCCTCAC GCAGGACCCT AGGAGCCCCG GACATTTTCT CAGGAACATC AGACACAGGC 881  
 TCCCTGCCAC CCAACCTCCA GCCTGCATAT TCTCCTTCCC CAACCCATCC TCCTACTGGA 941  
 CAGTATACGC TCTTCCCTCT TCCACCCACC TTGCCACCC CTGTGGTCCA GCTCCACCCC 1001  
 CTGCTTCCTG ACCCTTCTGC TCCAACGCCC ACCCCTACCA GCCCTCTTCT AAACACATCC 1061  
 TACACCCACT CCCAGAATCT GTCTCAGGAA GGGTAAGGTT CTCAGACACT GCCGACATCA 1121  
 GCATTGTCTC GTGTACAGCT CCCTTCCCTG CAGGCGCCCC CTGGGAGACA ACTGGACAAG 1181  
 ATTTCTTACT TTCTCCTGAA ACCCAAAGCC CTGGTAAAG GGATACACAG GACTGAAAAG 1241  
 GGAATCATTT TTTACTGTAC ATTATAAACC TTCAGAAGCT ATTTTTTTTAA GCTATCAGCA 1301  
 ATACTCATCA GAGCAGCTAG CTCTTTGGTC TATTTTCTGC A 1342

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
 1 5 10 15  
 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
 20 25 30  
 His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
 35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
50 55 60

Gly Ala Val Thr Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
65 70 75 80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln  
85 90 95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu  
100 105 110

Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe  
115 120 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
130 135 140

Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala  
145 150 155 160

Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu  
165 170

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGAGCCAC GCCAGCCAGA CACCCCGGCC AGAATGGAGC TGACTGAATT GCTCCTCGTG 60

GTCATGCTTC TCCTAACTGC AAGGCTAACG CTGTCC AGC CCG GCT CCT CCT GCT 114  
Ser Pro Ala Pro Pro Ala  
1 5

TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT 162  
Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu  
10 15 20

CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT 210  
His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro  
25 30 35

GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG 258  
 Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln  
 40 45 50  
 ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG 306  
 Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu  
 55 60 65 70  
 CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC 354  
 Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu  
 75 80 85  
 TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG 402  
 Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly  
 90 95 100  
 GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC 450  
 Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr  
 105 110 115  
 ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG 498  
 Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu  
 120 125 130  
 CTC CGA GGA AAG GAC TTC TGG ATT GTT GGA GAC AAA CTT CAC TGC CTC 546  
 Leu Arg Gly Lys Asp Phe Trp Ile Val Gly Asp Lys Leu His Cys Leu  
 135 140 145 150  
 AGC CAG AAC TAC TGG CTC TGG GCT TCT GAA GTG GCA GCA GGG ATT CAG 594  
 Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu Val Ala Ala Gly Ile Gln  
 155 160 165  
 AGC CAA GAT TCC TGG TCT GCT GAA CCA AAC CTC CAG GTC CCT GGA CCA 642  
 Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn Leu Gln Val Pro Gly Pro  
 170 175 180  
 AAT CCC CGG ATA CCT GAA CAG GAT ACA CGA ACT CTT GAA TGG AAC TCG 690  
 Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg Thr Leu Glu Trp Asn Ser  
 185 190 195  
 TGG ACT CTT TCC TGG ACC CTC ACG CAG GAC CCT AGG AGC CCC GGA CAT 738  
 Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp Pro Arg Ser Pro Gly His  
 200 205 210  
 TTC CTC AGG AAC ATC AGA CAC AGG CTC CCT GCC ACC CAA CCT CCA GCC 786  
 Phe Leu Arg Asn Ile Arg His Arg Leu Pro Ala Thr Gln Pro Pro Ala  
 215 220 225 230  
 TGG ATA TTC TCC TTC CCC AAC CCA TCC TCC TAC TGG ACA GTA TAC GCT 834  
 Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser Tyr Trp Thr Val Tyr Ala  
 235 240 245  
 CTT CCC TCT TCC ACC CAC CTT GCC CAC CCC TGT GGT CCA GCT CCA CCC 882  
 Leu Pro Ser Ser Thr His Leu Ala His Pro Cys Gly Pro Ala Pro Pro  
 250 255 260

CCT GCT TCC TGACCCTTCT GCTCCAACGC CCACCCCTAC CAGCCCTCTT 931  
 Pro Ala Ser  
 265

CTAAACACAT CCTACACCOA CTCCCAGAAT CTGTCTCAGG AAGGGTAAGG TTCTCAGACA 991  
 CTGCCGACAT CAGCATTGTC TCGTGTACAG CTCCCTTCCC TGCAGGGCGC CCCTGGGAGA 1051  
 CAACTGGACA AGATTTCTTA CTTTCTCCTG AAACCCAAAG CCCTGGTAAA AGGGATACAC 1111  
 AGGACTGAAA AGGGAATCAT TTTTCACTGT ACATTATAAA CCTTCAGAAG CTA 1164

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
 1 5 10 15

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
 20 25 30

His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
 35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
 50 55 60

Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
 65 70 75 80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln  
 85 90 95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu  
 100 105 110

Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe  
 115 120 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Asp Phe Trp Ile Val Gly  
 130 135 140

Asp Lys Leu His Cys Leu Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu  
 145 150 155 160

Val Ala Ala Gly Ile Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn  
 165 170 175



Leu Gln Val Pro Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg  
 180 185 190  
 Thr Leu Glu Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp  
 195 200 205  
 Pro Arg Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro  
 210 215 220  
 Ala Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser  
 225 230 235 240  
 Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His Pro  
 245 250 255  
 Cys Gly Pro Ala Pro Pro Pro Ala Ser  
 260 265

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCTCACTA GTGTCGACCT GCAG

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCAGGTCG AACTAGTGA GCTC

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCATAATTT TTAAAAAATT CATTTGACAA ATGCTAAAT TCTTGATTAA TATTCTCAAT 60  
TGTGAGCGCT CACAATTTAT 80

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGATAAATTG TGAGCGCTCA CAATTGAGAA TATTAATCAA GAATTTTAGC ATTTGTCAAA 60  
TGAATTTTTT AAAAATTATG AGACGT 86

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GACGTCTCAT AATTTTTTAAA AAATTCATT GACAAATGCT AAAATTCTTG ATTAATATTC 60  
TCAATTGTGA GCGCTCACAA TTTATCGAT 89